



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANT: ALBERTSEN, HANS  
ANAND, RAKESH  
CARLSON, MARY  
GRODEN, JOANNA  
HEDGE, PHILIP J.  
JOSLYN, GEOFF  
KINZLER, KENNETH  
MARKHAM, ALEXANDER F.  
NAKAMURA, YUSUKE  
THLIVERIS, ANDREW  
VOGELSTEIN, BERT  
WHITE, RAYMOND L.

(ii) TITLE OF INVENTION: APC ANTIBODIES

(iii) NUMBER OF SEQUENCES: [102] 154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Banner & Allegretti, LTD  
(B) STREET: 1001 G Street, NW  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20001-4598

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

((vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/442,489  
(B) FILING DATE: 18-NOV-1999  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/452,654  
(B) FILING DATE: 25-MAY-1995

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/289,548  
(B) FILING DATE: 12-AUG-1994

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/741,940  
(B) FILING DATE: 08-AUG-1001

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A.  
(B) REGISTRATION NUMBER: 32,141  
(C) REFERENCE/DOCKET NUMBER: 1107.035574

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-508-9100  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 9606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(vii) IMMEDIATE SOURCE:

(B) CLONE: DP2.5 (APC)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 34..8562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGACTCGGAA ATGAGGTCCA AGGGTAGCCA AGG ATG GCT GCA GCT TCA TAT GAT	54	
Met Ala Ala Ala Ser Tyr Asp		
1	5	
CAG TTG TTA AAG CAA GTT GAG GCA CTG AAG ATG GAG AAC TCA AAT CTT	102	
Gln Leu Leu Lys Gln Val Glu Ala Leu Lys Met Glu Asn Ser Asn Leu		
10	15	20
CGA CAA GAG CTA GAA GAT AAT TCC AAT CAT CTT ACA AAA CTG GAA ACT	150	
Arg Gln Glu Leu Glu Asp Asn Ser Asn His Leu Thr Lys Leu Glu Thr		
25	30	35
GAG GCA TCT AAT ATG AAG GAA GTA CTT AAA CAA CTA CAA GGA AGT ATT	198	
Glu Ala Ser Asn Met Lys Glu Val Leu Lys Gln Leu Gln Gly Ser Ile		

40	45	50	55	
GAA GAT GAA GCT ATG GCT TCT TCT GGA CAG ATT GAT TTA TTA GAG CGT Glu Asp Glu Ala Met Ala Ser Ser Gly Gln Ile Asp Leu Leu Glu Arg				246
60	65	70		
CTT AAA GAG CTT AAC TTA GAT AGC AGT AAT TTC CCT GGA GTA AAA CTG Leu Lys Glu Leu Asn Leu Asp Ser Ser Asn Phe Pro Gly Val Lys Leu				294
75	80	85		
CGG TCA AAA ATG TCC CTC CGT TCT TAT GGA AGC CGG GAA GGA TCT GTA Arg Ser Lys Met Ser Leu Arg Ser Tyr Gly Ser Arg Glu Gly Ser Val				342
90	95	100		
TCA AGC CGT TCT GGA GAG TGC AGT CCT GTT CCT ATG GGT TCA TTT CCA Ser Ser Arg Ser Gly Glu Cys Ser Pro Val Pro Met Gly Ser Phe Pro				390
105	110	115		
AGA AGA GGG TTT GTA AAT GGA AGC AGA GAA AGT ACT GGA TAT TTA GAA Arg Arg Gly Phe Val Asn Gly Ser Arg Glu Ser Thr Gly Tyr Leu Glu				438
120	125	130	135	
GAA CTT GAG AAA GAG AGG TCA TTG CTT CTT GCT GAT CTT GAC AAA GAA Glu Leu Glu Lys Glu Arg Ser Leu Leu Leu Ala Asp Leu Asp Lys Glu				486
140	145	150		
GAA AAG GAA AAA GAC TGG TAT TAC GCT CAA CTT CAG AAT CTC ACT AAA Glu Lys Glu Lys Asp Trp Tyr Ala Gln Leu Gln Asn Leu Thr Lys				534
155	160	165		
AGA ATA GAT AGT CTT CCT TTA ACT GAA AAT TTT TCC TTA CAA ACA GAT Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr Asp				582
170	175	180		
TTG ACC AGA AGG CAA TTG GAA TAT GAA GCA AGG CAA ATC AGA GTT GCG Leu Thr Arg Arg Gln Leu Glu Tyr Glu Ala Arg Gln Ile Arg Val Ala				630
185	190	195		
ATG GAA GAA CAA CTA GGT ACC TGC CAG GAT ATG GAA AAA CGA GCA CAG Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala Gln				678
200	205	210	215	
CGA AGA ATA GCC AGA ATT CAG CAA ATC GAA AAG GAC ATA CTT CGT ATA Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu Lys Asp Ile Leu Arg Ile				726
220	225	230		
CGA CAG CTT TTA CAG TCC CAA GCA ACA GAA GCA GAG AGG TCA TCT CAG Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu Ala Glu Arg Ser Ser Gln				774
235	240	245		
AAC AAG CAT GAA ACC GGC TCA CAT GAT GCT GAG CGG CAG AAT GAA GGT				822

Asn Lys His Glu Thr Gly Ser His Asp Ala Glu Arg Gln Asn Glu Gly			
250	255	260	
CAA GGA GTG GGA GAA ATC AAC ATG GCA ACT TCT GGT AAT GGT CAG GGT			870
Gln Gly Val Gly Glu Ile Asn Met Ala Thr Ser Gly Asn Gly Gln Gly			
265	270	275	
TCA ACT ACA CGA ATG GAC CAT GAA ACA GCC AGT GTT TTG AGT TCT AGT			918
Ser Thr Thr Arg Met Asp His Glu Thr Ala Ser Val Leu Ser Ser Ser			
280	285	290	295
AGC ACA CAC TCT GCA CCT CGA AGG CTG ACA AGT CAT CTG GGA ACC AAG			966
Ser Thr His Ser Ala Pro Arg Arg Leu Thr Ser His Leu Gly Thr Lys			
300	305	310	
GTG GAA ATG GTG TAT TCA TTG TTG TCA ATG CTT GGT ACT CAT GAT AAG			1014
Val Glu Met Val Tyr Ser Leu Leu Ser Met Leu Gly Thr His Asp Lys			
315	320	325	
GAT GAT ATG TCG CGA ACT TTG CTA GCT ATG TCT AGC TCC CAA GAC AGC			1062
Asp Asp Met Ser Arg Thr Leu Leu Ala Met Ser Ser Ser Gln Asp Ser			
330	335	340	
TGT ATA TCC ATG CGA CAG TCT GGA TGT CTT CCT CTC CTC ATC CAG CTT			1110
Cys Ile Ser Met Arg Gln Ser Gly Cys Leu Pro Leu Leu Ile Gln Leu			
345	350	355	
TTA CAT GGC AAT GAC AAA GAC TCT GTA TTG TTG GGA AAT TCC CGG GGC			1158
Leu His Gly Asn Asp Lys Asp Ser Val Leu Leu Gly Asn Ser Arg Gly			
360	365	370	375
AGT AAA GAG GCT CGG GCC AGG GCC AGT GCA GCA CTC CAC AAC ATC ATT			1206
Ser Lys Glu Ala Arg Ala Ser Ala Ala Leu His Asn Ile Ile			
380	385	390	
CAC TCA CAG CCT GAT GAC AAG AGA GGC AGG CGT GAA ATC CGA GTC CTT			1254
His Ser Gln Pro Asp Asp Lys Arg Gly Arg Arg Glu Ile Arg Val Leu			
395	400	405	
CAT CTT TTG GAA CAG ATA CGC GCT TAC TGT GAA ACC TGT TGG GAG TGG			1302
His Leu Leu Glu Gln Ile Arg Ala Tyr Cys Glu Thr Cys Trp Glu Trp			
410	415	420	
CAG GAA GCT CAT GAA CCA GGC ATG GAC CAG GAC AAA AAT CCA ATG CCA			1350
Gln Glu Ala His Glu Pro Gly Met Asp Gln Asp Lys Asn Pro Met Pro			
425	430	435	
GCT CCT GTT GAA CAT CAG ATC TGT CCT GCT GTG TGT GTT CTA ATG AAA			1398
Ala Pro Val Glu His Gln Ile Cys Pro Ala Val Cys Val Leu Met Lys			
440	445	450	455

CTT TCA TTT GAT GAA GAG CAT AGA CAT GCA ATG AAT GAA CTA GGG GGA Leu Ser Phe Asp Glu Glu His Arg His Ala Met Asn Glu Leu Gly Gly 460 465 470	1446
CTA CAG GCC ATT GCA GAA TTA TTG CAA GTG GAC TGT GAA ATG TAT GGG Leu Gln Ala Ile Ala Glu Leu Leu Gln Val Asp Cys Glu Met Tyr Gly 475 480 485	1494
CTT ACT AAT GAC CAC TAC AGT ATT ACA CTA AGA CGA TAT GCT GGA ATG Leu Thr Asn Asp His Tyr Ser Ile Thr Leu Arg Arg Tyr Ala Gly Met 490 495 500	1542
GCT TTG ACA AAC TTG ACT TTT GGA GAT GTA GCC AAC AAG GCT ACG CTA Ala Leu Thr Asn Leu Thr Phe Gly Asp Val Ala Asn Lys Ala Thr Leu 505 510 515	1590
TGC TCT ATG AAA GGC TGC ATG AGA GCA CTT GTG GCC CAA CTA AAA TCT Cys Ser Met Lys Gly Cys Met Arg Ala Leu Val Ala Gln Leu Lys Ser 520 525 530 535	1638
GAA AGT GAA GAC TTA CAG CAG GTT ATT GCA AGT GTT TTG AGG AAT TTG Glu Ser Glu Asp Leu Gln Gln Val Ile Ala Ser Val Leu Arg Asn Leu 540 545 550	1686
TCT TGG CGA GCA GAT GTA AAT AGT AAA AAG ACG TTG CGA GAA GTT GGA Ser Trp Arg Ala Asp Val Asn Ser Lys Lys Thr Leu Arg Glu Val Gly 555 560 565	1734
AGT GTG AAA GCA TTG ATG GAA TGT GCT TTA GAA GTT AAA AAG GAA TCA Ser Val Lys Ala Leu Met Glu Cys Ala Leu Glu Val Lys Lys Glu Ser 570 575 580	1782
ACC CTC AAA AGC GTA TTG AGT GCC TTA TGG AAT TTG TCA GCA CAT TGC Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn Leu Ser Ala His Cys 585 590 595	1830
ACT GAG AAT AAA GCT GAT ATA TGT GCT GTA GAT GGT GCA CTT GCA TTT Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asp Gly Ala Leu Ala Phe 600 605 610 615	1878
TTG GTT GGC ACT CTT ACT TAC CGG AGC CAG ACA AAC ACT TTA GCC ATT Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln Thr Asn Thr Leu Ala Ile 620 625 630	1926
ATT GAA AGT GGA GGT GGG ATA TTA CGG AAT GTG TCC AGC TTG ATA GCT Ile Glu Ser Gly Gly Ile Leu Arg Asn Val Ser Ser Leu Ile Ala 635 640 645	1974
ACA AAT GAG GAC CAC AGG CAA ATC CTA AGA GAG AAC AAC TGT CTA CAA Thr Asn Glu Asp His Arg Gln Ile Leu Arg Glu Asn Asn Cys Leu Gln 650 655 660	2022

ACT TTA TTA CAA CAC TTA AAA TCT CAT AGT TTG ACA ATA GTC AGT AAT Thr Leu Leu Gln His Leu Lys Ser His Ser Leu Thr Ile Val Ser Asn	665	670	675	2070
GCA TGT GGA ACT TTG TGG AAT CTC TCA GCA AGA AAT CCT AAA GAC CAG Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg Asn Pro Lys Asp Gln	680	685	690	695
GAA GCA TTA TGG GAC ATG GGG GCA GTT AGC ATG CTC AAG AAC CTC ATT Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met Leu Lys Asn Leu Ile	700	705	710	2166
CAT TCA AAG CAC AAA ATG ATT GCT ATG GGA AGT GCT GCA GCT TTA AGG His Ser Lys His Lys Met Ile Ala Met Gly Ser Ala Ala Ala Leu Arg	715	720	725	2214
AAT CTC ATG GCA AAT AGG CCT GCG AAG TAC AAG GAT GCC AAT ATT ATG Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr Lys Asp Ala Asn Ile Met	730	735	740	2262
TCT CCT GGC TCA AGC TTG CCA TCT CTT CAT GTT AGG AAA CAA AAA GCC Ser Pro Gly Ser Ser Leu Pro Ser Leu His Val Arg Lys Gln Lys Ala	745	750	755	2310
CTA GAA GCA GAA TTA GAT GCT CAG CAC TTA TCA GAA ACT TTT GAC AAT Leu Glu Ala Glu Leu Asp Ala Gln His Leu Ser Glu Thr Phe Asp Asn	760	765	770	775
ATA GAC AAT TTA AGT CCC AAG GCA TCT CAT CGT AGT AAG CAG AGA CAC Ile Asp Asn Leu Ser Pro Lys Ala Ser His Arg Ser Lys Gln Arg His	780	785	790	2406
AAG CAA AGT CTC TAT GGT GAT TAT GTT TTT GAC ACC AAT CGA CAT GAT Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe Asp Thr Asn Arg His Asp	795	800	805	2454
GAT AAT AGG TCA GAC AAT TTT AAT ACT GGC AAC ATG ACT GTC CTT TCA Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly Asn Met Thr Val Leu Ser	810	815	820	2502
CCA TAT TTG AAT ACT ACA GTG TTA CCC AGC TCC TCT TCA TCA AGA GGA Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser Ser Ser Arg Gly	825	830	835	2550
AGC TTA GAT AGT TCT CGT TCT GAA AAA GAT AGA AGT TTG GAG AGA GAA Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp Arg Ser Leu Glu Arg Glu	840	845	850	855
				2598

CGC GGA ATT GGT CTA GGC AAC TAC CAT CCA GCA ACA GAA AAT CCA GGA Arg Gly Ile Gly Leu Gly Asn Tyr His Pro Ala Thr Glu Asn Pro Gly 860 865 870	2646
ACT TCT TCA AAG CGA GGT TTG CAG ATC TCC ACC ACT GCA GCC CAG ATT Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser Thr Thr Ala Ala Gln Ile 875 880 885	2694
GCC AAA GTC ATG GAA GAA GTG TCA GCC ATT CAT ACC TCT CAG GAA GAC Ala Lys Val Met Glu Glu Val Ser Ala Ile His Thr Ser Gln Glu Asp 890 895 900	2742
AGA AGT TCT GGG TCT ACC ACT GAA TTA CAT TGT GTG ACA GAT GAG AGA Arg Ser Ser Gly Ser Thr Thr Glu Leu His Cys Val Thr Asp Glu Arg 905 910 915	2790
AAT GCA CTT AGA AGA AGC TCT GCT GCC CAT ACA CAT TCA AAC ACT TAC Asn Ala Leu Arg Arg Ser Ser Ala Ala His Thr His Ser Asn Thr Tyr 920 925 930 935	2838
AAT TTC ACT AAG TCG GAA AAT TCA AAT AGG ACA TGT TCT ATG CCT TAT Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg Thr Cys Ser Met Pro Tyr 940 945 950	2886
GCC AAA TTA GAA TAC AAG AGA TCT TCA AAT GAT AGT TTA AAT AGT GTC Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn Asp Ser Leu Asn Ser Val 955 960 965	2934
AGT AGT AAT GAT GGT TAT GGT AAA AGA GGT CAA ATG AAA CCC TCG ATT Ser Ser Asn Asp Gly Tyr Gly Lys Arg Gly Gln Met Lys Pro Ser Ile 970 975 980	2982
GAA TCC TAT TCT GAA GAT GAT GAA AGT AAG TTT TGC AGT TAT GGT CAA Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys Phe Cys Ser Tyr Gly Gln 985 990 995	3030
TAC CCA GCC GAC CTA GCC CAT AAA ATA CAT AGT GCA AAT CAT ATG GAT Tyr Pro Ala Asp Leu Ala His Lys Ile His Ser Ala Asn His Met Asp 1000 1005 1010 1015	3078
GAT AAT GAT GGA GAA CTA GAT ACA CCA ATA AAT TAT AGT CTT AAA TAT Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile Asn Tyr Ser Leu Lys Tyr 1020 1025 1030	3126
TCA GAT GAG CAG TTG AAC TCT GGA AGG CAA AGT CCT TCA CAG AAT GAA Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln Ser Pro Ser Gln Asn Glu 1035 1040 1045	3174
AGA TGG GCA AGA CCC AAA CAC ATA ATA GAA GAT GAA ATA AAA CAA AGT Arg Trp Ala Arg Pro Lys His Ile Ile Glu Asp Glu Ile Lys Gln Ser 1050 1055 1060	3222

GAG CAA AGA CAA TCA AGG AAT CAA AGT ACA ACT TAT CCT GTT TAT ACT Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr Thr Tyr Pro Val Tyr Thr 1065 1070 1075	3270
GAG AGC ACT GAT GAT AAA CAC CTC AAG TTC CAA CCA CAT TTT GGA CAG Glu Ser Thr Asp Asp Lys His Leu Lys Phe Gln Pro His Phe Gly Gln 1080 1085 1090 1095	3318
CAG GAA TGT GTT TCT CCA TAC AGG TCA CGG GGA GCC AAT GGT TCA GAA Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg Gly Ala Asn Gly Ser Glu 1100 1105 1110	3366
ACA AAT CGA GTG GGT TCT AAT CAT GGA ATT AAT CAA AAT GTA AGC CAG Thr Asn Arg Val Gly Ser Asn His Gly Ile Asn Gln Asn Val Ser Gln 1115 1120 1125	3414
TCT TTG TGT CAA GAA GAT GAC TAT GAA GAT GAT AAG CCT ACC AAT TAT Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp Asp Lys Pro Thr Asn Tyr 1130 1135 1140	3462
AGT GAA CGT TAC TCT GAA GAA CAG CAT GAA GAA GAA GAG AGA CCA Ser Glu Arg Tyr Ser Glu Glu Gln His Glu Glu Glu Glu Arg Pro 1145 1150 1155	3510
ACA AAT TAT AGC ATA AAA TAT AAT GAA GAG AAA CGT CAT GTG GAT CAG Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu Lys Arg His Val Asp Gln 1160 1165 1170 1175	3558
CCT ATT GAT TAT AGT TTA AAA TAT GCC ACA GAT ATT CCT TCA TCA CAG Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr Asp Ile Pro Ser Ser Gln 1180 1185 1190	3606
AAA CAG TCA TTT TCA TTC TCA AAG AGT TCA TCT GGA CAA AGC AGT AAA Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser Ser Gly Gln Ser Ser Lys 1195 1200 1205	3654
ACC GAA CAT ATG TCT TCA AGC AGT GAG AAT ACG TCC ACA CCT TCA TCT Thr Glu His Met Ser Ser Ser Glu Asn Thr Ser Thr Pro Ser Ser 1210 1215 1220	3702
AAT GCC AAG AGG CAG AAT CAG CTC CAT CCA AGT TCT GCA CAG AGT AGA Asn Ala Lys Arg Gln Asn Gln Leu His Pro Ser Ser Ala Gln Ser Arg 1225 1230 1235	3750
AGT GGT CAG CCT CAA AAG GCT GCC ACT TGC AAA GTT TCT TCT ATT AAC Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys Lys Val Ser Ser Ile Asn 1240 1245 1250 1255	3798

CAA GAA ACA ATA CAG ACT TAT TGT GTA GAA GAT ACT CCA ATA TGT TTT Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe 1260 1265 1270	3846
TCA AGA TGT AGT TCA TTA TCA TCT TTG TCA TCA GCT GAA GAT GAA ATA Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser Ala Glu Asp Glu Ile 1275 1280 1285	3894
GGA TGT AAT CAG ACG ACA CAG GAA GCA GAT TCT GCT AAT ACC CTG CAA Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp Ser Ala Asn Thr Leu Gln 1290 1295 1300	3942
ATA GCA GAA ATA AAA GGA AAG ATT GGA ACT AGG TCA GCT GAA GAT CCT Ile Ala Glu Ile Lys Gly Lys Ile Gly Thr Arg Ser Ala Glu Asp Pro 1305 1310 1315	3990
GTG AGC GAA GTT CCA GCA GTG TCA CAG CAC CCT AGA ACC AAA TCC AGC Val Ser Glu Val Pro Ala Val Ser Gln His Pro Arg Thr Lys Ser Ser 1320 1325 1330 1335	4038
AGA CTG CAG GGT TCT AGT TTA TCT TCA GAA TCA GCC AGG CAC AAA GCT Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu Ser Ala Arg His Lys Ala 1340 1345 1350	4086
GTT GAA TTT CCT TCA GGA GCG AAA TCT CCC TCC AAA AGT GGT GCT CAG Val Glu Phe Pro Ser Gly Ala Lys Ser Pro Ser Lys Ser Gly Ala Gln 1355 1360 1365	4134
ACA CCC AAA AGT CCA CCT GAA CAC TAT GTT CAG GAG ACC CCA CTC ATG Thr Pro Lys Ser Pro Pro Glu His Tyr Val Gln Glu Thr Pro Leu Met 1370 1375 1380	4182
TTT AGC AGA TGT ACT TCT GTC AGT TCA CTT GAT AGT TTT GAG AGT CGT Phe Ser Arg Cys Thr Ser Val Ser Ser Leu Asp Ser Phe Glu Ser Arg 1385 1390 1395	4230
TCG ATT GCC AGC TCC GTT CAG AGT GAA CCA TGC AGT GGA ATG GTA AGT Ser Ile Ala Ser Ser Val Gln Ser Glu Pro Cys Ser Gly Met Val Ser 1400 1405 1410 1415	4278
GGC ATT ATA AGC CCC AGT GAT CTT CCA GAT AGC CCT GGA CAA ACC ATG Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp Ser Pro Gly Gln Thr Met 1420 1425 1430	4326
CCA CCA AGC AGA AGT AAA ACA CCT CCA CCA CCT CCT CAA ACA GCT CAA Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro Pro Gln Thr Ala Gln 1435 1440 1445	4374
ACC AAG CGA GAA GTA CCT AAA AAT AAA GCA CCT ACT GCT GAA AAG AGA Thr Lys Arg Glu Val Pro Lys Asn Lys Ala Pro Thr Ala Glu Lys Arg 1450 1455 1460	4422

GAG AGT GGA CCT AAG CAA GCT GCA GTA AAT GCT GCA GTT CAG AGG GTC Glu Ser Gly Pro Lys Gln Ala Ala Val Asn Ala Ala Val Gln Arg Val 1465 1470 1475	4470
CAG GTT CTT CCA GAT GCT GAT ACT TTA TTA CAT TTT GCC ACA GAA AGT Gln Val Leu Pro Asp Ala Asp Thr Leu Leu His Phe Ala Thr Glu Ser 1480 1485 1490 1495	4518
ACT CCA GAT GGA TTT TCT TGT TCA TCC AGC CTG AGT GCT CTG AGC CTC Thr Pro Asp Gly Phe Ser Cys Ser Ser Leu Ser Ala Leu Ser Leu 1500 1505 1510	4566
GAT GAG CCA TTT ATA CAG AAA GAT GTG GAA TTA AGA ATA ATG CCT CCA Asp Glu Pro Phe Ile Gln Lys Asp Val Glu Leu Arg Ile Met Pro Pro 1515 1520 1525	4614
GTT CAG GAA AAT GAC AAT GGG AAT GAA ACA GAA TCA GAG CAG CCT AAA Val Gln Glu Asn Asp Asn Gly Asn Glu Thr Glu Ser Glu Gln Pro Lys 1530 1535 1540	4662
GAA TCA AAT GAA AAC CAA GAG AAA GAG GCA GAA AAA ACT ATT GAT TCT Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala Glu Lys Thr Ile Asp Ser 1545 1550 1555	4710
GAA AAG GAC CTA TTA GAT GAT TCA GAT GAT GAT ATT GAA ATA CTA Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp Asp Ile Glu Ile Leu 1560 1565 1570 1575	4758
GAA GAA TGT ATT ATT TCT GCC ATG CCA ACA AAG TCA TCA CGT AAA GGC Glu Glu Cys Ile Ile Ser Ala Met Pro Thr Lys Ser Ser Arg Lys Gly 1580 1585 1590	4806
AAA AAG CCA GCC CAG ACT GCT TCA AAA TTA CCT CCA CCT GTG GCA AGG Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu Pro Pro Pro Val Ala Arg 1595 1600 1605	4854
AAA CCA AGT CAG CTG CCT GTG TAC AAA CTT CTA CCA TCA CAA AAC AGG Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu Leu Pro Ser Gln Asn Arg 1610 1615 1620	4902
TTG CAA CCC CAA AAG CAT GTT AGT TTT ACA CCG GGG GAT GAT ATG CCA Leu Gln Pro Gln Lys His Val Ser Phe Thr Pro Gly Asp Asp Met Pro 1625 1630 1635	4950
CGG GTG TAT TGT GTT GAA GGG ACA CCT ATA AAC TTT TCC ACA GCT ACA Arg Val Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr 1640 1645 1650 1655	4998

TCT CTA AGT GAT CTA ACA ATC GAA TCC CCT CCA AAT GAG TTA GCT GCT Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro Pro Asn Glu Leu Ala Ala 1660 1665 1670	5046
GGA GAA GGA GTT AGA GGA GGA GCA CAG TCA GGT GAA TTT GAA AAA CGA Gly Glu Gly Val Arg Gly Ala Gln Ser Gly Glu Phe Glu Lys Arg 1675 1680 1685	5094
GAT ACC ATT CCT ACA GAA GGC AGA AGT ACA GAT GAG GCT CAA GGA GGA Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr Asp Glu Ala Gln Gly Gly 1690 1695 1700	5142
AAA ACC TCA TCT GTA ACC ATA CCT GAA TTG GAT GAC AAT AAA GCA GAG Lys Thr Ser Ser Val Thr Ile Pro Glu Leu Asp Asp Asn Lys Ala Glu 1705 1710 1715	5190
GAA GGT GAT ATT CTT GCA GAA TGC ATT AAT TCT GCT ATG CCC AAA GGG Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn Ser Ala Met Pro Lys Gly 1720 1725 1730 1735	5238
AAA AGT CAC AAG CCT TTC CGT GTG AAA AAG ATA ATG GAC CAG GTC CAG Lys Ser His Lys Pro Phe Arg Val Lys Ile Met Asp Gln Val Gln 1740 1745 1750	5286
CAA GCA TCT GCG TCG TCT TCT GCA CCC AAC AAA AAT CAG TTA GAT GGT Gln Ala Ser Ala Ser Ser Ala Pro Asn Lys Asn Gln Leu Asp Gly 1755 1760 1765	5334
AAG AAA AAG AAA CCA ACT TCA CCA GTA AAA CCT ATA CCA CAA AAT ACT Lys Lys Lys Pro Thr Ser Pro Val Lys Pro Ile Pro Gln Asn Thr 1770 1775 1780	5382
GAA TAT AGG ACA CGT GTA AGA AAA AAT GCA GAC TCA AAA AAT AAT TTA Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala Asp Ser Lys Asn Asn Leu 1785 1790 1795	5430
AAT GCT GAG AGA GTT TTC TCA GAC AAC AAA GAT TCA AAG AAA CAG AAT Asn Ala Glu Arg Val Phe Ser Asp Asn Lys Asp Ser Lys Lys Gln Asn 1800 1805 1810 1815	5478
TTG AAA AAT AAT TCC AAG GAC TTC AAT GAT AAG CTC CCA AAT AAT GAA Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp Lys Leu Pro Asn Asn Glu 1820 1825 1830	5526
GAT AGA GTC AGA GGA AGT TTT GCT TTT GAT TCA CCT CAT CAT TAC ACG Asp Arg Val Arg Gly Ser Phe Ala Phe Asp Ser Pro His His Tyr Thr 1835 1840 1845	5574
CCT ATT GAA GGA ACT CCT TAC TGT TTT TCA CGA AAT GAT TCT TTG AGT Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu Ser 1850 1855 1860	5622

TCT CTA GAT TTT GAT GAT GAT GAT GTT GAC CTT TCC AGG GAA AAG GCT Ser Leu Asp Phe Asp Asp Asp Val Asp Leu Ser Arg Glu Lys Ala 1865 1870 1875	5670
GAA TTA AGA AAG GCA AAA GAA AAT AAG GAA TCA GAG GCT AAA GTT ACC Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu Ser Glu Ala Lys Val Thr 1880 1885 1890 1895	5718
AGC CAC ACA GAA CTA ACC TCC AAC CAA CAA TCA GCT AAT AAG ACA CAA Ser His Thr Glu Leu Thr Ser Asn Gln Gln Ser Ala Asn Lys Thr Gln 1900 1905 1910	5766
GCT ATT GCA AAG CAG CCA ATA AAT CGA GGT CAG CCT AAA CCC ATA CTT Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly Gln Pro Lys Pro Ile Leu 1915 1920 1925	5814
CAG AAA CAA TCC ACT TTT CCC CAG TCA TCC AAA GAC ATA CCA GAC AGA Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser Lys Asp Ile Pro Asp Arg 1930 1935 1940	5862
GGG GCA GCA ACT GAT GAA AAG TTA CAG AAT TTT GCT ATT GAA AAT ACT Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn Phe Ala Ile Glu Asn Thr 1945 1950 1955	5910
CCA GTT TGC TTT TCT CAT AAT TCC TCT CTG AGT TCT CTC AGT GAC ATT Pro Val Cys Phe Ser His Asn Ser Ser Leu Ser Ser Leu Ser Asp Ile 1960 1965 1970 1975	5958
GAC CAA GAA AAC AAC AAT AAA GAA AAT GAA CCT ATC AAA GAG ACT GAG Asp Gln Glu Asn Asn Lys Glu Asn Glu Pro Ile Lys Glu Thr Glu 1980 1985 1990	6006
CCC CCT GAC TCA CAG GGA GAA CCA AGT AAA CCT CAA GCA TCA GGC TAT Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys Pro Gln Ala Ser Gly Tyr 1995 2000 2005	6054
GCT CCT AAA TCA TTT CAT GTT GAA GAT ACC CCA GTT TGT TTC TCA AGA Ala Pro Lys Ser Phe His Val Glu Asp Thr Pro Val Cys Phe Ser Arg 2010 2015 2020	6102
AAC AGT TCT CTC AGT TCT CTT AGT ATT GAC TCT GAA GAT GAC CTG TTG Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp Ser Glu Asp Asp Leu Leu 2025 2030 2035	6150
CAG GAA TGT ATA AGC TCC GCA ATG CCA AAA AAG AAA AAG CCT TCA AGA Gln Glu Cys Ile Ser Ser Ala Met Pro Lys Lys Lys Pro Ser Arg 2040 2045 2050 2055	6198

CTC AAG GGT GAT AAT GAA AAA CAT AGT CCC AGA AAT ATG GGT GGC ATA Leu Lys Gly Asp Asn Glu Lys His Ser Pro Arg Asn Met Gly Gly Ile 2060 2065 2070	6246
TTA GGT GAA GAT CTG ACA CTT GAT TTG AAA GAT ATA CAG AGA CCA GAT Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys Asp Ile Gln Arg Pro Asp 2075 2080 2085	6294
TCA GAA CAT GGT CTA TCC CCT GAT TCA GAA AAT TTT GAT TGG AAA GCT Ser Glu His Gly Leu Ser Pro Asp Ser Glu Asn Phe Asp Trp Lys Ala 2090 2095 2100	6342
ATT CAG GAA GGT GCA AAT TCC ATA GTA AGT AGT TTA CAT CAA GCT GCT Ile Gln Glu Gly Ala Asn Ser Ile Val Ser Ser Leu His Gln Ala Ala 2105 2110 2115	6390
GCT GCT GCA TGT TTA TCT AGA CAA GCT TCG TCT GAT TCA GAT TCC ATC Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser Ser Asp Ser Asp Ser Ile 2120 2125 2130 2135	6438
CTT TCC CTG AAA TCA GGA ATC TCT CTG GGA TCA CCA TTT CAT CTT ACA Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly Ser Pro Phe His Leu Thr 2140 2145 2150	6486
CCT GAT CAA GAA GAA AAA CCC TTT ACA AGT AAT AAA GGC CCA CGA ATT Pro Asp Gln Glu Lys Pro Phe Thr Ser Asn Lys Gly Pro Arg Ile 2155 2160 2165	6534
CTA AAA CCA GGG GAG AAA AGT ACA TTG GAA ACT AAA AAG ATA GAA TCT Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu Thr Lys Lys Ile Glu Ser 2170 2175 2180	6582
GAA AGT AAA GGA ATC AAA GGA GGA AAA AAA GTT TAT AAA AGT TTG ATT Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys Val Tyr Lys Ser Leu Ile 2185 2190 2195	6630
ACT GGA AAA GTT CGA TCT AAT TCA GAA ATT TCA GGC CAA ATG AAA CAG Thr Gly Lys Val Arg Ser Asn Ser Glu Ile Ser Gly Gln Met Lys Gln 2200 2205 2210 2215	6678
CCC CTT CAA GCA AAC ATG CCT TCA ATC TCT CGA GGC AGG ACA ATG ATT Pro Leu Gln Ala Asn Met Pro Ser Ile Ser Arg Gly Arg Thr Met Ile 2220 2225 2230	6726
CAT ATT CCA GGA GTT CGA AAT AGC TCC TCA AGT ACA AGT CCT GTT TCT His Ile Pro Gly Val Arg Asn Ser Ser Ser Thr Ser Pro Val Ser 2235 2240 2245	6774
AAA AAA GGC CCA CCC CTT AAG ACT CCA GCC TCC AAA AGC CCT AGT GAA Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala Ser Lys Ser Pro Ser Glu 2250 2255 2260	6822

GGT CAA ACA GCC ACC ACT TCT CCT AGA GGA GCC AAG CCA TCT GTG AAA			6870
Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly Ala Lys Pro Ser Val Lys			
2265	2270	2275	
TCA GAA TTA AGC CCT GTT GCC AGG CAG ACA TCC CAA ATA GGT GGG TCA			6918
Ser Glu Leu Ser Pro Val Ala Arg Gln Thr Ser Gln Ile Gly Gly Ser			
2280	2285	2290	2295
AGT AAA GCA CCT TCT AGA TCA GGA TCT AGA GAT TCG ACC CCT TCA AGA			6966
Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg Asp Ser Thr Pro Ser Arg			
2300	2305	2310	
CCT GCC CAG CAA CCA TTA AGT AGA CCT ATA CAG TCT CCT GGC CGA AAC			7014
Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile Gln Ser Pro Gly Arg Asn			
2315	2320	2325	
TCA ATT TCC CCT GGT AGA AAT GGA ATA AGT CCT CCT AAC AAA TTA TCT			7062
Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser Pro Pro Asn Lys Leu Ser			
2330	2335	2340	
CAA CTT CCA AGG ACA TCA TCC CCT AGT ACT GCT TCA ACT AAG TCC TCA			7110
Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr Ala Ser Thr Lys Ser Ser			
2345	2350	2355	
GGT TCT GGA AAA ATG TCA TAT ACA TCT CCA GGT AGA CAG ATG AGC CAA			7158
Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro Gly Arg Gln Met Ser Gln			
2360	2365	2370	2375
CAG AAC CTT ACC AAA CAA ACA GGT TTA TCC AAG AAT GCC AGT AGT ATT			7206
Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser Lys Asn Ala Ser Ser Ile			
2380	2385	2390	
CCA AGA AGT GAG TCT GCC TCC AAA GGA CTA AAT CAG ATG AAT AAT GGT			7254
Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu Asn Gln Met Asn Asn Gly			
2395	2400	2405	
AAT GGA GCC AAT AAA AAG GTA GAA CTT TCT AGA ATG TCT TCA ACT AAA			7302
Asn Gly Ala Asn Lys Lys Val Glu Leu Ser Arg Met Ser Ser Thr Lys			
2410	2415	2420	
TCA AGT GGA AGT GAA TCT GAT AGA TCA GAA AGA CCT GTA TTA GTA CGC			7350
Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu Arg Pro Val Leu Val Arg			
2425	2430	2435	
CAG TCA ACT TTC ATC AAA GAA GCT CCA AGC CCA ACC TTA AGA AGA AAA			7398
Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser Pro Thr Leu Arg Arg Lys			
2440	2445	2450	2455

TTG GAG GAA TCT GCT TCA TTT GAA TCT CTT TCT CCA TCA TCT AGA CCA Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu Ser Pro Ser Ser Arg Pro 2460	2465	2470	7446
GCT TCT CCC ACT AGG TCC CAG GCA CAA ACT CCA GTT TTA AGT CCT TCC Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr Pro Val Leu Ser Pro Ser 2475	2480	2485	7494
CTT CCT GAT ATG TCT CTA TCC ACA CAT TCG TCT GTT CAG GCT GGT GGA Leu Pro Asp Met Ser Leu Ser Thr His Ser Ser Val Gln Ala Gly Gly 2490	2495	2500	7542
TGG CGA AAA CTC CCA CCT AAT CTC AGT CCC ACT ATA GAG TAT AAT GAT Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro Thr Ile Glu Tyr Asn Asp 2505	2510	2515	7590
GGA AGA CCA GCA AAG CGC CAT GAT ATT GCA CGG TCT CAT TCT GAA AGT Gly Arg Pro Ala Lys Arg His Asp Ile Ala Arg Ser His Ser Glu Ser 2520	2525	2530	7638
CCT TCT AGA CTT CCA ATC AAT AGG TCA GGA ACC TGG AAA CGT GAG CAC Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly Thr Trp Lys Arg Glu His 2540	2545	2550	7686
AGC AAA CAT TCA TCA TCC CTT CCT CGA GTA AGC ACT TGG AGA AGA ACT Ser Lys His Ser Ser Ser Leu Pro Arg Val Ser Thr Trp Arg Arg Thr 2555	2560	2565	7734
GGA AGT TCA TCT TCA ATT CTT TCT GCT TCA TCA GAA TCC AGT GAA AAA Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser Ser Glu Ser Ser Glu Lys 2570	2575	2580	7782
GCA AAA AGT GAG GAT GAA AAA CAT GTG AAC TCT ATT TCA GGA ACC AAA Ala Lys Ser Glu Asp Glu Lys His Val Asn Ser Ile Ser Gly Thr Lys 2585	2590	2595	7830
CAA AGT AAA GAA AAC CAA GTA TCC GCA AAA GGA ACA TGG AGA AAA ATA Gln Ser Lys Glu Asn Gln Val Ser Ala Lys Gly Thr Trp Arg Lys Ile 2600	2605	2610	7878
AAA GAA AAT GAA TTT TCT CCC ACA AAT AGT ACT TCT CAG ACC GTT TCC Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser Thr Ser Gln Thr Val Ser 2620	2625	2630	7926
TCA GGT GCT ACA AAT GGT GCT GAA TCA AAG ACT CTA ATT TAT CAA ATG Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys Thr Leu Ile Tyr Gln Met 2635	2640	2645	7974
GCA CCT GCT GTT TCT AAA ACA GAG GAT GTT TGG GTG AGA ATT GAG GAC Ala Pro Ala Val Ser Lys Thr Glu Asp Val Trp Val Arg Ile Glu Asp 2650	2655	2660	8022

TGT CCC ATT AAC AAT CCT AGA TCT GGA AGA TCT CCC ACA GGT AAT ACT Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg Ser Pro Thr Gly Asn Thr 2665 2670 2675	8070
CCC CCG GTG ATT GAC AGT GTT TCA GAA AAG GCA AAT CCA AAC ATT AAA Pro Pro Val Ile Asp Ser Val Ser Glu Lys Ala Asn Pro Asn Ile Lys 2680 2685 2690 2695	8118
GAT TCA AAA GAT AAT CAG GCA AAA CAA AAT GTG GGT AAT GGC AGT GTT Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn Val Gly Asn Gly Ser Val 2700 2705 2710	8166
CCC ATG CGT ACC GTG GGT TTG GAA AAT CGC CTG ACC TCC TTT ATT CAG Pro Met Arg Thr Val Gly Leu Glu Asn Arg Leu Thr Ser Phe Ile Gln 2715 2720 2725	8214
GTG GAT GCC CCT GAC CAA AAA GGA ACT GAG ATA AAA CCA GGA CAA AAT Val Asp Ala Pro Asp Gln Lys Gly Thr Glu Ile Lys Pro Gly Gln Asn 2730 2735 2740	8262
AAT CCT GTC CCT GTA TCA GAG ACT AAT GAA AGT CCT ATA GTG GAA CGT Asn Pro Val Pro Val Ser Glu Thr Asn Glu Ser Pro Ile Val Glu Arg 2745 2750 2755	8310
ACC CCA TTC AGT TCT AGC AGC TCA AGC AAA CAC AGT TCA CCT AGT GGG Thr Pro Phe Ser Ser Ser Ser Lys His Ser Ser Pro Ser Gly 2760 2765 2770 2775	8358
ACT GTT GCT GCC AGA GTG ACT CCT TTT AAT TAC AAC CCA AGC CCT AGG Thr Val Ala Ala Arg Val Thr Pro Phe Asn Tyr Asn Pro Ser Pro Arg 2780 2785 2790	8406
AAA AGC AGC GCA GAT AGC ACT TCA GCT CGG CCA TCT CAG ATC CCA ACT Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg Pro Ser Gln Ile Pro Thr 2795 2800 2805	8454
CCA GTG AAT AAC ACA AAG CGA GAT TCC AAA ACT GAC AGC ACA Pro Val Asn Asn Asn Thr Lys Lys Arg Asp Ser Lys Thr Asp Ser Thr 2810 2815 2820	8502
GAA TCC AGT GGA ACC CAA AGT CCT AAG CGC CAT TCT GGG TCT TAC CTT Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg His Ser Gly Ser Tyr Leu 2825 2830 2835	8550
GTG ACA TCT GTT TAAAAGAGAG GAAGAATGAA ACTAAGAAAA TTCTATGTTA Val Thr Ser Val 2840	8602
ATTACAAC TG CTATATAGAC ATTTTGTTC AAATGAAACT TTAAAAGACT GAAAAATT GTAAATAGGT TTGATTCTTG TTAGAGGGTT TTTGTTCTGG AAGCCATATT TGATAGTATA	8662
	8722

CTTTGTCTTC ACTGGTCTTA TTTTGGGAGG CACTCTGAT GGTTAGGAAA AAATAGAAAG	8782
CCAAGTATGT TTGTACAGTA TGTTTACAT GTATTAAAG TAGCATCCCA TCCCAACTTC	8842
CTTAATTATT GCTTGTCTAA ATAATGAAC ACTACAGATA GGAAATATGA TATATTGCTG	8902
TTATCAATCA TTTCTAGATT ATAAACTGAC TAAACTTACA TCAGGGGAAA ATTGGTATT	8962
ATGCAAAAAA AAAATGTTT TGTCTTG TGTCCTTG AGTCCATCTA ACATCATAAT TAATCATGTG	9022
GCTGTGAAAT TCACAGTAAT ATGGTTCCCG ATGAACAAGT TTACCCAGCC TGCTTGCTT	9082
ACTGCATGAA TGAAACTGAT GGTTCAATT CAGAAGTAAT GATTAACAGT TATGTGGTCA	9142
CATGATGTGC ATAGAGATAG CTACAGTGT AATAATTACA CTATTTGTG CTCCAAACAA	9202
AACAAAAATC TGTGTAAC TG TAAACATTG AATGAAACTA TTTTACCTGA ACTAGATT	9262
ATCTGAAAGT AGGTAGAATT TTTGCTATGC TGTAAATTGT TGTATATTCT GGTATTGAG	9322
GTGAGATGGC TGCTCTTAT TAATGAGACA TGAATTGTGT CTCAACAGAA ACTAAATGAA	9382
CATTTCAGAA TAAATTATTG CTGTATGTAA ACTGTTACTG AAATTGGTAT TTGTTGAAG	9442
GGTTTGTTC ACATTGTAT TAATTAATTG TTTAAAATGC CTCTTTAAA AGCTTATATA	9502
AATTTTTCT TCAGCTTCTA TGCATTAAGA GTAAAATTCC TCTTACTGT AAAAAACAT	9562
TGAAGAAGAC TGTTGCCACT TAACCATTCC ATGCGTTGGC ACTT	9606

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2843 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu  
 1                5                10                15

Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn  
 20                25                30

His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu  
 35                40                45

Lys	Gln	Leu	Gln	Gly	Ser	Ile	Glu	Asp	Glu	Ala	Met	Ala	Ser	Ser	Gly
50						55					60				
Gln	Ile	Asp	Leu	Leu	Glu	Arg	Leu	Lys	Glu	Leu	Asn	Leu	Asp	Ser	Ser
65						70					75			80	
Asn	Phe	Pro	Gly	Val	Lys	Leu	Arg	Ser	Lys	Met	Ser	Leu	Arg	Ser	Tyr
				85					90				95		
Gly	Ser	Arg	Glu	Gly	Ser	Val	Ser	Ser	Arg	Ser	Gly	Glu	Cys	Ser	Pro
						100		105				110			
Val	Pro	Met	Gly	Ser	Phe	Pro	Arg	Arg	Gly	Phe	Val	Asn	Gly	Ser	Arg
						115		120				125			
Glu	Ser	Thr	Gly	Tyr	Leu	Glu	Glu	Leu	Glu	Lys	Glu	Arg	Ser	Leu	Leu
					130		135			140					
Leu	Ala	Asp	Leu	Asp	Lys	Glu	Glu	Lys	Glu	Lys	Asp	Trp	Tyr	Tyr	Ala
					145		150			155			160		
Gln	Leu	Gln	Asn	Leu	Thr	Lys	Arg	Ile	Asp	Ser	Leu	Pro	Leu	Thr	Glu
					165				170				175		
Asn	Phe	Ser	Leu	Gln	Thr	Asp	Leu	Thr	Arg	Arg	Gln	Leu	Glu	Tyr	Glu
					180			185				190			
Ala	Arg	Gln	Ile	Arg	Val	Ala	Met	Glu	Glu	Gln	Leu	Gly	Thr	Cys	Gln
					195		200			205					
Asp	Met	Glu	Lys	Arg	Ala	Gln	Arg	Arg	Ile	Ala	Arg	Ile	Gln	Gln	Ile
					210		215			220					
Glu	Lys	Asp	Ile	Leu	Arg	Ile	Arg	Gln	Leu	Leu	Gln	Ser	Gln	Ala	Thr
					225		230			235			240		
Glu	Ala	Glu	Arg	Ser	Ser	Gln	Asn	Lys	His	Glu	Thr	Gly	Ser	His	Asp
					245			250			255				
Ala	Glu	Arg	Gln	Asn	Glu	Gly	Gln	Gly	Val	Gly	Glu	Ile	Asn	Met	Ala
					260		265			270					
Thr	Ser	Gly	Asn	Gly	Gln	Gly	Ser	Thr	Thr	Arg	Met	Asp	His	Glu	Thr
					275		280			285					
Ala	Ser	Val	Leu	Ser	Ser	Ser	Ser	Thr	His	Ser	Ala	Pro	Arg	Arg	Leu
					290		295			300					
Thr	Ser	His	Leu	Gly	Thr	Lys	Val	Glu	Met	Val	Tyr	Ser	Leu	Leu	Ser
					305		310			315			320		

Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala  
325 330 335

Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys  
340 345 350

Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val  
355 360 365

Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser  
370 375 380

Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly  
385 390 395 400

Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr  
405 410 415

Cys Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp  
420 425 430

Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro  
435 440 445

Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His  
450 455 460

Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln  
465 470 475 480

Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr  
485 490 495

Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp  
500 505 510

Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala  
515 520 525

Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile  
530 535 540

Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys  
545 550 555 560

Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala  
565 570 575

Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu  
580 585 590

Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala  
595 600 605

Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser  
610 615 620

Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg  
625 630 640

Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu  
645 650 655

Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His  
660 665 670

Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser  
675 680 685

Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val  
690 695 700

Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met  
705 710 715 720

Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys  
725 730 735

Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu  
740 745 750

His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His  
755 760 765

Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser  
770 775 780

His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val  
785 790 795 800

Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr  
805 810 815

Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro  
820 825 830

Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys  
835 840 845

Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His  
850 855 860

Pro	Ala	Thr	Glu	Asn	Pro	Gly	Thr	Ser	Ser	Lys	Arg	Gly	Leu	Gln	Ile
865					870					875					880
Ser	Thr	Thr	Ala	Ala	Gln	Ile	Ala	Lys	Val	Met	Glu	Glu	Val	Ser	Ala
			885					890						895	
Ile	His	Thr	Ser	Gln	Glu	Asp	Arg	Ser	Ser	Gly	Ser	Thr	Thr	Glu	Leu
	900							905						910	
His	Cys	Val	Thr	Asp	Glu	Arg	Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala
	915				920							925			
His	Thr	His	Ser	Asn	Thr	Tyr	Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn
	930					935					940				
Arg	Thr	Cys	Ser	Met	Pro	Tyr	Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser
	945				950					955				960	
Asn	Asp	Ser	Leu	Asn	Ser	Val	Ser	Ser	Asn	Asp	Gly	Tyr	Gly	Lys	Arg
			965						970				975		
Gly	Gln	Met	Lys	Pro	Ser	Ile	Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser
			980					985					990		
Lys	Phe	Cys	Ser	Tyr	Gly	Gln	Tyr	Pro	Ala	Asp	Leu	Ala	His	Lys	Ile
	995						1000					1005			
His	Ser	Ala	Asn	His	Met	Asp	Asp	Asn	Asp	Gly	Glu	Leu	Asp	Thr	Pro
	1010					1015						1020			
Ile	Asn	Tyr	Ser	Leu	Lys	Tyr	Ser	Asp	Glu	Gln	Leu	Asn	Ser	Gly	Arg
	1025					1030				1035				1040	
Gln	Ser	Pro	Ser	Gln	Asn	Glu	Arg	Trp	Ala	Arg	Pro	Lys	His	Ile	Ile
					1045				1050				1055		
Glu	Asp	Glu	Ile	Lys	Gln	Ser	Glu	Gln	Arg	Gln	Ser	Arg	Asn	Gln	Ser
			1060					1065				1070			
Thr	Thr	Tyr	Pro	Val	Tyr	Thr	Glu	Ser	Thr	Asp	Asp	Lys	His	Leu	Lys
			1075				1080					1085			
Phe	Gln	Pro	His	Phe	Gly	Gln	Gln	Glu	Cys	Val	Ser	Pro	Tyr	Arg	Ser
	1090					1095					1100				
Arg	Gly	Ala	Asn	Gly	Ser	Glu	Thr	Asn	Arg	Val	Gly	Ser	Asn	His	Gly
	1105					1110				1115				1120	
Ile	Asn	Gln	Asn	Val	Ser	Gln	Ser	Leu	Cys	Gln	Glu	Asp	Asp	Tyr	Glu
				1125					1130				1135		

Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Gln  
1140 1145 1150

His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu  
1155 1160 1165

Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala  
1170 1175 1180

Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser  
1185 1190 1195 1200

Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu  
1205 1210 1215

Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His  
1220 1225 1230

Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr  
1235 1240 1245

Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val  
1250 1255 1260

Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu  
1265 1270 1275 1280

Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala  
1285 1290 1295

Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Gly Lys Ile Gly  
1300 1305 1310

Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln  
1315 1320 1325

His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser  
1330 1335 1340

Glu Ser Ala Arg His Lys Ala Val Glu Phe Pro Ser Gly Ala Lys Ser  
1345 1350 1355 1360

Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr  
1365 1370 1375

Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser  
1380 1385 1390

Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu  
1395 1400 1405

Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro  
1410 1415 1420

Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro  
1425 1430 1435 1440

Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys  
1445 1450 1455

Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val  
1460 1465 1470

Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu  
1475 1480 1485

Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser  
1490 1495 1500

Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val  
1505 1510 1515 1520

Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu  
1525 1530 1535

Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu  
1540 1545 1550

Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp  
1555 1560 1565

Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ser Ala Met Pro  
1570 1575 1580

Thr Lys Ser Ser Arg Lys Gly Lys Lys Pro Ala Gln Thr Ala Ser Lys  
1585 1590 1595 1600

Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys  
1605 1610 1615

Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe  
1620 1625 1630

Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro  
1635 1640 1645

Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser  
1650 1655 1660

Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln  
1665 1670 1675 1680

Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser  
1685 1690 1695

Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu  
1700 1705 1710

Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile  
1715 1720 1725

Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys  
1730 1735 1740

Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro  
1745 1750 1755 1760

Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val  
1765 1770 1775

Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn  
1780 1785 1790

Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn  
1795 1800 1805

Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn  
1810 1815 1820

Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe  
1825 1830 1835 1840

Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe  
1845 1850 1855

Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Asp Val  
1860 1865 1870

Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys  
1875 1880 1885

Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln  
1890 1895 1900

Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg  
1905 1910 1915 1920

Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser  
1925 1930 1935

Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln  
1940 1945 1950

Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser  
1955 1960 1965

Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn  
1970 1975 1980

Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser  
1985 1990 1995 2000

Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp  
2005 2010 2015

Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile  
2020 2025 2030

Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro  
2035 2040 2045

Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser  
2050 2055 2060

Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu  
2065 2070 2075 2080

Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser  
2085 2090 2095

Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val  
2100 2105 2110

Ser Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala  
2115 2120 2125

Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu  
2130 2135 2140

Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr  
2145 2150 2155 2160

Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu  
2165 2170 2175

Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys  
2180 2185 2190

Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu  
2195 2200 2205

Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile  
2210 2215 2220

Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser  
2225 2230 2235 2240

Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro  
2245 2250 2255

Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg  
2260 2265 2270

Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln  
2275 2280 2285

Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser  
2290 2295 2300

Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro  
2305 2310 2315 2320

Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile  
2325 2330 2335

Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser  
2340 2345 2350

Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser  
2355 2360 2365

Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu  
2370 2375 2380

Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly  
2385 2390 2395 2400

Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu  
2405 2410 2415

Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser  
2420 2425 2430

Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro  
2435 2440 2445

Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser  
2450 2455 2460

Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln  
2465 2470 2475 2480

Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His  
2485 2490 2495

Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser  
2500 2505 2510

Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile  
2515 2520 2525

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser  
2530 2535 2540

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg  
2545 2550 2555 2560

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ile Leu Ser Ala  
2565 2570 2575

Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val  
2580 2585 2590

Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala  
2595 2600 2605

Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn  
2610 2615 2620

Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser  
2625 2630 2635 2640

Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp  
2645 2650 2655

Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly  
2660 2665 2670

Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu  
2675 2680 2685

Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln  
2690 2695 2700

Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn  
2705 2710 2715 2720

Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr  
2725 2730 2735

Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn  
2740 2745 2750

Glu Ser Pro Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser  
2755 2760 2765

Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe  
2770 2775 2780

Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala  
2785 2790 2795 2800

Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg  
2805 2810 2815

Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys  
2820 2825 2830

Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val  
2835 2840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DP1(TB2)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCA GTC GCC GCT CCA GTC TAT CCG GCA CTA GGA ACA GCC CCG GGN GGC 48  
Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly  
1 5 10 15

GAG ACG GTC CCC GCC ATG TCT GCG GCC ATG AGG GAG AGG TTC GAC CGG 96  
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg  
20 25 30

TTC CTG CAC GAG AAG AAC TGC ATG ACT GAC CTT CTG GCC AAG CTC GAG 144  
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu  
35 40 45

GCC AAA ACC GGC GTG AAC AGC AGC TTC ATC GCT CTT GGT GTC ATC GGA Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly	50	55	60	192
CTG GTG GCC TTG TAC CTG GTG TTC GGT TAT GGA GCC TCT CTC CTC TGC Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys	65	70	75	240
AAC CTG ATA GGA TTT GGC TAC CCA GCC TAC TCA ATT AAA GCT ATA Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile	85	90	95	288
GAG AGT CCC AAC AAA GAA GAT GAT ACC CAG TGG CTG ACC TAC TGG GTA Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val	100	105	110	336
GTG TAT GGT GTG TTC AGC ATT GCT GAA TTC TTC TCT GAT ATC TTC CTG Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu	115	120	125	384
TCA TGG TTC CCC TTC TAC TAC ATG CTG AAG TGT GGC TTC CTG TTG TGG Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp	130	135	140	432
TGC ATG GCC CCG AGC CCT TCT AAT GGG GCT GAA CTG CTC TAC AAG CGC Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg	145	150	155	480
ATC ATC CGT CCT TTC CTG AAG CAC GAG TCC CAG ATG GAC AGT GTG Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val	165	170	175	528
GTC AAG GAC CTT AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr	180	185	190	576
AAA GAA GCG AAG AAA GCT ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys	195	200	205	624
AGC ACC TAAACCAGAC TAAACCAGAC TGGATGGAAA CTTCTGCC CTCCTGTACC Ser Thr	210			680
TTCCTACTGG AGCTTGATGT TATATTAGGG ACTGTGGTAT AATTATTTA ATAATGTTGC				740
CTTGGAAACA TTTTGAGAT ATTAAAGATT GGAATGTGTT GTAAGTTCT TTGCTTACTT				800
TTACTGTCTA TATATATAGG GAGCACTTTA AACTTAATGC AGTGGGCAGT GTCCACGTTT				860
TTGGAAAATG TATTTGCCT CTGGGTAGGA AAAGATGTAT GTTGCTATCC TGCAGGAAAT				920

ATAAAACCTTAA	AATAAAATTA	TATACCCCAC	AGGCTGTGTA	CTTTACTGGG	CTCTCCCTGC	980
ACGSATTTC	TCTGTAGTTA	CATTTAGGRT	AATCTTTATG	GTTCTACTTC	CTRATAATGTA	1040
CAATTTATA	TAATTNCNGRA	ATGTTTTAA	TGTATTGTG	CACATGTACA	TATGGAAATG	1100
TTACTGTCTG	ACTACANCAT	GCATCATGCT	CATGGGGAGG	GAGCAGGGGA	AGGTTGTATG	1160
TGTCATTTAT	AACTTCTGTA	CAGTAAGACC	ACCTGCCAAA	AGCTGGAGGA	ACCATTGTGC	1220
TGGTGTGGTC	TACTAAATAA	TACTTTAGGA	AATACGTGAT	TAATATGCAA	GTGAACAAAG	1280
TGAGAAATGA	AATCGAATGG	AGATTGGCCT	GGTTGTTCC	GTAGTATATG	GCATATGAAT	1340
ACCAGGATAG	CTTTATAAAG	CAGTTAGTTA	GTTAGTTACT	CACTCTAGTG	ATAAATCGGG	1400
AAATTTACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAG	1460
AGTACCCGT	AACTCTCAAT	TCCCTGAAAA	ACTAGTAATA	CTGTCTTATC	TGCTATAAAC	1520
TTTACATATT	TGTCTATTGT	CAAGATGCTA	CANTGGAMNC	CATTCTGGT	TTTATCTTCA	1580
NAGSGGAGAN	ACATGTTGAT	TTAGTCTTCT	TTCCCAATCT	TCTTTTTAA	MCCAGTTNA	1640
GGMNCTTCTG	RAGATTGTYC	CACCTCTGAT	TACATGTATG	TTCTYGTTG	TATCATKAGC	1700
AACAACATGC	TAATGRGCAC	ACCTAGCTCT	RAGMGCAATT	CTGGGAGANT	GARAGGNWGT	1760
ATARAGTMNC	CCATAATCTG	CTTGGCAATA	GTAAAGTC	TCTATCTTCA	GTTTTCTCT	1820
GGCCTTTAAG	GTCAAACACA	AGAGGCTTCC	CTAGTTACA	AGTCAGAGTC	ACTTGTAGTC	1880
CATTTAAATG	CCCTCATCCG	TATTCTTTGT	GTTGATAAGC	TGCACAKGAC	TACATAGTAA	1940
GTACAGANCA	GTAAAGTTAA	NNCGGATGTC	TCCATTGATC	TGCCAANTCG	NTATAGAGAG	2000
CAATTTGTCT	GGACTAGAAA	ATCTGAGTTT	TACACCATA	TGTTAAGAGT	CCTTTGAAT	2060
TAAACTAGAC	TAAAACAAGT	GTATAACTAA	ACTAACAAAGA	TTAAATATCC	AGCCAGTACA	2120
GTATTTTTA	AGGCAAATAA	AGATGATTAG	CTCACCTTGA	GNTAACAAATC	AGGTAAGATC	2180
ATNACAATGT	CTCATGATGT	NAANAATATT	AAAGATATCA	ATACTAAGTG	ACAGTATCAC	2240
NNCTAATATA	ATATGGATCA	GAGCATTAT	TTGGGGAGG	AAAACAGTGG	TGATTACCGG	2300
CATTTTATTA	AACTAAAAC	TTTGTAGAAA	GCAAACAAAA	TTGTTCTTGG	GAGAAAATCA	2360
ACTTTTAGAT	TAAAAAAATT	TTAAGTAWCT	AGGAGTATT	AAATCCTTT	CCCATAAATA	2420

AAAGTACAGT TTTCTTGGTG GCAGAATGAA AATCAGCAAC NTCTAGCATA TAGACTATAT	2480
AATCAGATTG ACAGCATATA GAATATATTA TCAGACAAGA TGAGGAGGTA CAAAAGTTAC	2540
TATTGCTCAT AATGACTTAC AGGCTAAAAN TAGNTNTAAA ATACTATATT AAATTCTGAA	2600
TGCAATTTTT TTTTGTTCCT TTGAGACCAA AATTAAAGTT AACTGTTGCT GGCAGTCTAA	2660
GTGTAAATGT TAACAGCAGG AGAAGTTAACG AATTGAGCAG TTCTGTTGCA TGATTCCCA	2720
AATGAAATAC TGCCTTGGCT AGAGTTGAA AAACTAATTG AGCCTGTGCC TGGCTAGAAA	2780
ACAAGCGTTT ATTTGAATGT GAATAGTGT TCAAAGGTAT GTAGTTACAG AATTCCCTACC	2840
AAACAGCTTA AATTCTCAA GAAAGAATTG CTGCAGCAGT TATTCCCTTA CCTGAAGGCT	2900
TCAATCATTG GGATCAACAA CTGCTACTCT CGGGAAAGACT CCTCTACTCA CAGCTGAAGA	2960
AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATCCTGAA GATGTGATAC ACTGAATGGA	3020
AATAAAATAGA TGTAAATAAA ATTGAGWTCT CATTAAAAAA AAACCATGTG CCCAATGGGA	3080
AAATGACCTC ATGTTGTGGT TTAAACAGCA ACTGCACCCA CTAGCACAGC CCATTGAGCT	3140
ANCCTATATA TACATCTCTG TCAGTGCCCC TC	3172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly			
1	5	10	15
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg			
20	25	30	
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu			
35	40	45	
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly			
50	55	60	
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys			

65	70	75	80
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile			
85		90	95
Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val			
100		105	110
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu			
115	120		125
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp			
130	135		140
Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg			
145	150		155
Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val			
165		170	175
Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr			
180		185	190
Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys			
195		200	205
Ser Thr			
210			

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 434 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 

- (B) CLONE: TB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Ala Pro Val Val Val	Gly Ser Gly Arg Ala Pro Arg His Pro Ala		
1	5	10	15

Pro	Ala	Ala	Met	His	Pro	Arg	Arg	Pro	Asp	Gly	Phe	Asp	Gly	Leu	Gly
			20					25						30	
Tyr	Arg	Gly	Gly	Ala	Arg	Asp	Glu	Gln	Gly	Phe	Gly	Gly	Ala	Phe	Pro
	35					40							45		
Ala	Arg	Ser	Phe	Ser	Thr	Gly	Ser	Asp	Leu	Gly	His	Trp	Val	Thr	Thr
		50				55					60				
Pro	Pro	Asp	Ile	Pro	Gly	Ser	Arg	Asn	Leu	His	Trp	Gly	Glu	Lys	Ser
	65					70			75				80		
Pro	Pro	Tyr	Gly	Val	Pro	Thr	Thr	Ser	Thr	Pro	Tyr	Glu	Gly	Pro	Thr
		85					90						95		
Glu	Glu	Pro	Phe	Ser	Ser	Gly	Gly	Gly	Ser	Val	Gln	Gly	Gln	Ser	
		100					105						110		
Ser	Glu	Gln	Leu	Asn	Arg	Phe	Ala	Gly	Phe	Gly	Ile	Gly	Leu	Ala	Ser
		115					120					125			
Leu	Phe	Thr	Glu	Asn	Val	Leu	Ala	His	Pro	Cys	Ile	Val	Leu	Arg	Arg
		130					135					140			
Gln	Cys	Gln	Val	Asn	Tyr	His	Ala	Gln	His	Tyr	His	Leu	Thr	Pro	Phe
	145				150				155					160	
Thr	Val	Ile	Asn	Ile	Met	Tyr	Ser	Phe	Asn	Lys	Thr	Gln	Gly	Pro	Arg
		165				170							175		
Ala	Leu	Trp	Lys	Gly	Met	Gly	Ser	Thr	Phe	Ile	Val	Gln	Gly	Val	Thr
		180					185					190			
Leu	Gly	Ala	Glu	Gly	Ile	Ile	Ser	Glu	Phe	Thr	Pro	Leu	Pro	Arg	Glu
		195					200					205			
Val	Leu	His	Lys	Trp	Ser	Pro	Lys	Gln	Ile	Gly	Glu	His	Leu	Leu	Leu
		210				215					220				
Lys	Ser	Leu	Thr	Tyr	Val	Val	Ala	Met	Pro	Phe	Tyr	Ser	Ala	Ser	Leu
	225				230				235				240		
Ile	Glu	Thr	Val	Gln	Ser	Glu	Ile	Ile	Arg	Asp	Asn	Thr	Gly	Ile	Leu
		245					250						255		
Glu	Cys	Val	Lys	Glu	Gly	Ile	Gly	Arg	Val	Ile	Gly	Met	Gly	Val	Pro
		260					265					270			
His	Ser	Lys	Arg	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Ile	Phe	Pro	Thr	Val
		275					280					285			

Leu His Gly Val Leu His Tyr Ile Ile Ser Ser Val Ile Gln Lys Phe  
290 295 300

Val Leu Leu Ile Leu Lys Arg Lys Thr Tyr Asn Ser His Leu Ala Glu  
305 310 315 320

Ser Thr Ser Pro Val Gln Ser Met Leu Asp Ala Tyr Phe Pro Glu Leu  
325 330 335

Ile Ala Asn Phe Ala Ala Ser Leu Cys Ser Asp Val Ile Leu Tyr Pro  
340 345 350

Leu Glu Thr Val Leu His Arg Leu His Ile Gln Gly Thr Arg Thr Ile  
355 360 365

Ile Asp Asn Thr Asp Leu Gly Tyr Glu Val Leu Pro Ile Asn Thr Gln  
370 375 380

Tyr Glu Gly Met Arg Asp Cys Ile Asn Thr Ile Arg Gln Glu Glu Gly  
385 390 395 400

Val Phe Gly Phe Tyr Lys Gly Phe Gly Ala Val Ile Ile Gln Tyr Thr  
405 410 415

Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu  
420 425 430

Leu Gln

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 185 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:  
(B) CLONE: YS-39(TB2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Leu	Arg	Arg	Phe	Asp	Arg	Phe	Leu	His	Glu	Lys	Asn	Cys	Met	Thr
1				5				10						15	
Asp	Leu	Leu	Ala	Lys	Leu	Glu	Ala	Lys	Thr	Gly	Val	Asn	Arg	Ser	Phe
				20				25						30	
Ile	Ala	Leu	Gly	Val	Ile	Gly	Leu	Val	Ala	Leu	Tyr	Leu	Val	Phe	Gly
				35				40						45	
Tyr	Gly	Ala	Ser	Leu	Leu	Cys	Asn	Leu	Ile	Gly	Phe	Gly	Tyr	Pro	Ala
				50				55						60	
Tyr	Ile	Ser	Ile	Lys	Ala	Ile	Glu	Ser	Pro	Asn	Lys	Glu	Asp	Asp	Thr
				65				70				75		80	
Gln	Trp	Leu	Thr	Tyr	Trp	Val	Val	Tyr	Gly	Val	Phe	Ser	Ile	Ala	Glu
				85				90						95	
Phe	Phe	Ser	Asp	Ile	Phe	Leu	Ser	Trp	Phe	Pro	Phe	Tyr	Tyr	Ile	Leu
				100				105						110	
Lys	Cys	Gly	Phe	Leu	Leu	Trp	Cys	Met	Ala	Pro	Ser	Pro	Ser	Asn	Gly
				115				120						125	
Ala	Glu	Leu	Leu	Tyr	Lys	Arg	Ile	Ile	Arg	Pro	Phe	Phe	Leu	Lys	His
				130				135						140	
Glu	Ser	Gln	Met	Asp	Ser	Val	Val	Lys	Asp	Leu	Lys	Asp	Lys	Ala	Lys
				145				150				155		160	
Glu	Thr	Ala	Asp	Ala	Ile	Thr	Lys	Glu	Ala	Lys	Lys	Ala	Thr	Val	Asn
				165				170						175	
Leu	Leu	Gly	Glu	Glu	Lys	Lys	Ser	Thr							
				180				185							

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: [2842] 2843 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 

- (B) CLONE: APC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu  
1 5 10 15

Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn  
20 25 30

His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu  
35 40 45

Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly  
50 55 60

Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser  
65 70 75 80

Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr  
85 90 95

Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro  
100 105 110

Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg  
115 120 125

Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu  
130 135 140

Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala  
145 150 155 160

Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu [Leu Thr Glu Asn  
165 170 175

Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala  
180 185 190

Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln Asp  
195 200 205

Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu  
210 215 220

Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu  
225 230 235 240

Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala

245	250	255	
Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr			
260	265	270	
Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala			
275	280	285	
Ser Val Leu Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr			
290	295	300	
Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met			
305	310	315	320
Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met			
325	330	335	
Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys Leu			
340	345	350	
Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val Leu			
355	360	365	
Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala			
370	375	380	
Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly Arg			
385	390	395	400
Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr Cys			
405	410	415	
Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp Gln			
420	425	430	
Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro Ala			
435	440	445	
Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His Ala			
450	455	460	
Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln Val			
465	470	475	480
Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr Leu			
485	490	495	
Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp Val			
500	505	510	
Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala Leu			

515	520	525
Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile Ala		
530	535	540
Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys Lys		
545	550	555
Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala Leu		
565	570	575
Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu Trp		
580	585	590
Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala Val		
595	600	605
Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln		
610	615	620
Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Ile Leu Arg Asn		
625	630	635
640		
Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu Arg		
645	650	655
Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His Ser		
660	665	670
Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala		
675	680	685
Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser		
690	695	700
Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly		
705	710	715
720		
Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr		
725	730	735
Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His		
740	745	750
Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu		
755	760	765
Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His		
770	775	780
Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe		

785	790	795	800
Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly			
805	810	815	
Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser			
820	825	830	
Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp			
835	840	845	
Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro			
850	855	860	
Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser			
865	870	875	880
Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile			
885	890	895	
His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His			
900	905	910	
Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His			
915	920	925	
Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg			
930	935	940	
Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn			
945	950	955	960
Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg Gly			
965	970	975	
Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys			
980	985	990	
Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile His			
995	1000	1005	
Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile			
1010	1015	1020	
Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln			
1025	1030	1035	1040
Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile Glu			
1045	1050	1055	
Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr			

1060	1065	1070
Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys Phe		
1075	1080	1085
Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg		
1090	1095	1100
Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly Ile		
1105	1110	1115
Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp		
1125	1130	1135
Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln His		
1140	1145	1150
Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu		
1155	1160	1165
Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr		
1170	1175	1180
Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser		
1185	1190	1195
Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu Asn		
1205	1210	1215
Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro		
1220	1225	1230
Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys		
1235	1240	1245
Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu		
1250	1255	1260
Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser		
1265	1270	1275
Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp		
1285	1290	1295
Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly Thr		
1300	1305	1310
Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His		
1315	1320	1325
Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu		

1330	1335	1340
Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro		
1345	1350	1355
1360		
Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val		
1365	1370	1375
Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu		
1380	1385	1390
Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro		
1395	1400	1405
Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp		
1410	1415	1420
Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro		
1425	1430	1435
1440		
Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala		
1445	1450	1455
Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn		
1460	1465	1470
Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu		
1475	1480	1485
His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser		
1490	1495	1500
Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val Glu		
1505	1510	1515
1520		
Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr		
1525	1530	1535
Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala		
1540	1545	1550
Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp		
1555	1560	1565
Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr		
1570	1575	1580
Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu		
1585	1590	1595
1600		
Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu		

1605	1610	1615
Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr		
1620	1625	1630
Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro Ile		
1635	1640	1645
Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro		
1650	1655	1660
Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Ala Gln Ser		
1665	1670	1675
Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr		
1685	1690	1695
Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu Leu		
1700	1705	1710
Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn		
1715	1720	1725
Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys Lys		
1730	1735	1740
Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn		
1745	1750	1755
Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val Lys		
1765	1770	1775
Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala		
1780	1785	1790
Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn Lys		
1795	1800	1805
Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp		
1810	1815	1820
Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe Asp		
1825	1830	1835
Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser		
1845	1850	1855
Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val Asp		
1860	1865	1870
Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu		

1875	1880	1885
Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln Gln 1890	1895	1900
Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly 1905	1910	1915
Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser 1925	1930	1935
Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn 1940	1945	1950
Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu 1955	1960	1965
Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu 1970	1975	1980
Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys 1985	1990	1995
Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr 2005	2010	2015
Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp 2020	2025	2030
Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys 2035	2040	2045
Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro 2050	2055	2060
Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys 2065	2070	2075
Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu 2085	2090	2095
Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser 2100	2105	2110
Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser 2115	2120	2125
Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly 2130	2135	2140
Ser Pro Phe His Leu Thr Pro Asp Gln Glu Lys Pro Phe Thr Ser		

2145	2150	2155	2160
Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu			
2165	2170	2175	
Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys			
2180	2185	2190	
Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile			
2195	2200	2205	
Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser			
2210	2215	2220	
Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser			
2225	2230	2235	2240
Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala			
2245	2250	2255	
Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly			
2260	2265	2270	
Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln Thr			
2275	2280	2285	
Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg			
2290	2295	2300	
Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile			
2305	2310	2315	2320
Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser			
2325	2330	2335	
Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr			
2340	2345	2350	
Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro			
2355	2360	2365	
Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser			
2370	2375	2380	
Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu			
2385	2390	2395	2400
Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser			
2405	2410	2415	
Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu			

2420	2425	2430
Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser		
2435	2440	2445
Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu		
2450	2455	2460
Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr		
2465	2470	2475
Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser		
2485	2490	2495
Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro		
2500	2505	2510
Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala		
2515	2520	2525
Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly		
2530	2535	2540
Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val		
2545	2550	2555
2560		
Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser		
2565	2570	2575
Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn		
2580	2585	2590
Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys		
2595	2600	2605
Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser		
2610	2615	2620
Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys		
2625	2630	2635
2640		
Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val		
2645	2650	2655
Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg		
2660	2665	2670
Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys		
2675	2680	2685
Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn		

2690	2695	2700
Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn Arg		
2705	2710	2715
Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr Glu		
2725	2730	2735
Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn Glu		
2740	2745	2750
Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Lys		
2755	2760	2765
His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe Asn		
2770	2775	2780
Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg		
2785	2790	2795
Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg Asp		
2805	2810	2815
Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg		
2820	2825	2830
His Ser Gly Ser Tyr Leu Val Thr Ser Val		
2835	2840 ]	
<u>Pro Leu Thr Glu</u>		
175		
<u>Asn Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu</u>		
180	185	190
<u>Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln</u>		
195	200	205
<u>Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile</u>		
210	215	220
<u>Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Gln Ser Gln Ala Thr</u>		
225	230	235
<u>Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp</u>		
245	250	255
<u>Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala</u>		
260	265	270
<u>Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr</u>		
275	280	285
<u>Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu</u>		
290	295	300
<u>Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser</u>		
305	310	315
<u>Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala</u>		
325	330	335

Met	Ser	Ser	Ser	Gln	Asp	Ser	Cys	Ile	Ser	Met	Arg	Gln	Ser	Gly	Cys
				340				345				350			
Leu	Pro	Leu	Leu	Ile	Gln	Leu	Leu	His	Gly	Asn	Asp	Lys	Asp	Ser	Val
				355				360				365			
Leu	Leu	Gly	Asn	Ser	Arg	Gly	Ser	Lys	Glu	Ala	Arg	Ala	Arg	Ala	Ser
				370				375				380			
Ala	Ala	Leu	His	Asn	Ile	Ile	His	Ser	Gln	Pro	Asp	Asp	Lys	Arg	Gly
				385				390				395			400
Arg	Arg	Glu	Ile	Arg	Val	Leu	His	Leu	Leu	Glu	Gln	Ile	Arg	Ala	Tyr
				405				410				415			
Cys	Glu	Thr	Cys	Trp	Glu	Trp	Gln	Glu	Ala	His	Pro	Gly	Met	Asp	
				420				425				430			
Gln	Asp	Lys	Asn	Pro	Met	Pro	Ala	Pro	Val	Glu	His	Gln	Ile	Cys	Pro
				435				440				445			
Ala	Val	Cys	Val	Leu	Met	Lys	Leu	Ser	Phe	Asp	Glu	Glu	His	Arg	His
				450				455				460			
Ala	Met	Asn	Glu	Leu	Gly	Gly	Leu	Gln	Ala	Ile	Ala	Glu	Leu	Leu	Gln
				465				470				475			480
Val	Asp	Cys	Glu	Met	Tyr	Gly	Leu	Thr	Asn	Asp	His	Tyr	Ser	Ile	Thr
				485				490				495			
Leu	Arg	Arg	Tyr	Ala	Gly	Met	Ala	Leu	Thr	Asn	Leu	Thr	Phe	Gly	Asp
				500				505				510			
Val	Ala	Asn	Lys	Ala	Thr	Leu	Cys	Ser	Met	Lys	Gly	Cys	Met	Arg	Ala
				515				520				525			
Leu	Val	Ala	Gln	Leu	Lys	Ser	Glu	Ser	Glu	Asp	Leu	Gln	Gln	Val	Ile
				530				535				540			
Ala	Ser	Val	Leu	Arg	Asn	Leu	Ser	Trp	Arg	Ala	Asp	Val	Asn	Ser	Lys
				545				550				555			560
Lys	Thr	Leu	Arg	Glu	Val	Gly	Ser	Val	Lys	Ala	Leu	Met	Glu	Cys	Ala
				565				570				575			
Leu	Glu	Val	Lys	Lys	Glu	Ser	Thr	Leu	Lys	Ser	Val	Leu	Ser	Ala	Leu
				580				585				590			
Trp	Asn	Leu	Ser	Ala	His	Cys	Thr	Glu	Asn	Lys	Ala	Asp	Ile	Cys	Ala
				595				600				605			
Val	Asp	Gly	Ala	Leu	Ala	Phe	Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser
				610				615				620			
Gln	Thr	Asn	Thr	Leu	Ala	Ile	Ile	Glu	Ser	Gly	Gly	Ile	Leu	Arg	
				625				630				635			640
Asn	Val	Ser	Ser	Leu	Ile	Ala	Thr	Asn	Glu	Asp	His	Arg	Gln	Ile	Leu
				645				650				655			
Arg	Glu	Asn	Asn	Cys	Leu	Gln	Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His
				660				665				670			
Ser	Leu	Thr	Ile	Val	Ser	Asn	Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser
				675				680				685			
Ala	Arg	Asn	Pro	Lys	Asp	Gln	Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val
				690				695				700			
Ser	Met	Leu	Lys	Asn	Leu	Ile	His	Ser	Lys	His	Lys	Met	Ile	Ala	Met
				705				710				715			720
Gly	Ser	Ala	Ala	Ala	Leu	Arg	Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys
				725				730				735			
Tyr	Lys	Asp	Ala	Asn	Ile	Met	Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu

740	745	750
His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His		
755	760	765
Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser		
770	775	780
His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val		
785	790	795
Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr		
805	810	815
Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro		
820	825	830
Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys		
835	840	845
Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His		
850	855	860
Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile		
865	870	875
Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala		
885	890	895
Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu		
900	905	910
His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala		
915	920	925
His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn		
930	935	940
Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser		
945	950	955
Asn Asp Ser Leu Asn Ser Val Ser Ser Asp Gly Tyr Gly Lys Arg		
965	970	975
Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser		
980	985	990
Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile		
995	1000	1005
His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro		
1010	1015	1020
Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg		
1025	1030	1035
Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile		
1045	1050	1055
Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser		
1060	1065	1070
Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys		
1075	1080	1085
Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser		
1090	1095	1100
Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly		
1105	1110	1115
Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu		
1125	1130	1135
Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Gln		
1140	1145	1150

<u>His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu</u>		
1155	1160	1165
<u>Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala</u>		
1170	1175	1180
<u>Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser</u>		
1185	1190	1195
<u>Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu</u>		
1205	1210	1215
<u>Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His</u>		
1220	1225	1230
<u>Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr</u>		
1235	1240	1245
<u>Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val</u>		
1250	1255	1260
<u>Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu</u>		
1265	1270	1275
<u>Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala</u>		
1285	1290	1295
<u>Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly</u>		
1300	1305	1310
<u>Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln</u>		
1315	1320	1325
<u>His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser</u>		
1330	1335	1340
<u>Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser</u>		
1345	1350	1355
<u>Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr</u>		
1365	1370	1375
<u>Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser</u>		
1380	1385	1390
<u>Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu</u>		
1395	1400	1405
<u>Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro</u>		
1410	1415	1420
<u>Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro</u>		
1425	1430	1435
<u>Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys</u>		
1445	1450	1455
<u>Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val</u>		
1460	1465	1470
<u>Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu</u>		
1475	1480	1485
<u>Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser</u>		
1490	1495	1500
<u>Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val</u>		
1505	1510	1515
<u>Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu</u>		
1525	1530	1535
<u>Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu</u>		
1540	1545	1550
<u>Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp</u>		

1555	1560	1565
Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro		
1570	1575	1580
Thr Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys		
1585	1590	1595
Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys		1600
1605	1610	1615
Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe		
1620	1625	1630
Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro		
1635	1640	1645
Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser		
1650	1655	1660
Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Ala Gln		
1665	1670	1675
Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser		
1685	1690	1695
Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu		
1700	1705	1710
Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile		
1715	1720	1725
Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys		
1730	1735	1740
Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ala Pro		
1745	1750	1755
Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val		
1765	1770	1775
Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn		
1780	1785	1790
Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn		
1795	1800	1805
Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn		
1810	1815	1820
Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe		
1825	1830	1835
Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe		
1845	1850	1855
Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val		
1860	1865	1870
Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys		
1875	1880	1885
Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln		
1890	1895	1900
Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg		
1905	1910	1915
Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser		
1925	1930	1935
Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln		
1940	1945	1950
Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser		
1955	1960	1965

<u>Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn</u>		
1970	1975	1980
<u>Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser</u>		
1985	1990	1995
<u>Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp</u>		
2005	2010	2015
<u>Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile</u>		
2020	2025	2030
<u>Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro</u>		
2035	2040	2045
<u>Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser</u>		
2050	2055	2060
<u>Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu</u>		
2065	2070	2075
<u>Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser</u>		
2085	2090	2095
<u>Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val</u>		
2100	2105	2110
<u>Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala</u>		
2115	2120	2125
<u>Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu</u>		
2130	2135	2140
<u>Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr</u>		
2145	2150	2155
<u>Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu</u>		
2165	2170	2175
<u>Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys</u>		
2180	2185	2190
<u>Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu</u>		
2195	2200	2205
<u>Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile</u>		
2210	2215	2220
<u>Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser</u>		
2225	2230	2235
<u>Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro</u>		
2245	2250	2255
<u>Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg</u>		
2260	2265	2270
<u>Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln</u>		
2275	2280	2285
<u>Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser</u>		
2290	2295	2300
<u>Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro</u>		
2305	2310	2315
<u>Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile</u>		
2325	2330	2335
<u>Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser</u>		
2340	2345	2350
<u>Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser</u>		
2355	2360	2365
<u>Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu</u>		

2370	2375	2380
Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly		
2385	2390	2395
Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu		
2405	2410	2415
Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser		
2420	2425	2430
Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro		
2435	2440	2445
Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser		
2450	2455	2460
Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln		
2465	2470	2475
Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His		
2485	2490	2495
Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser		
2500	2505	2510
Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile		
2515	2520	2525
Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser		
2530	2535	2540
Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg		
2545	2550	2555
Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ile Leu Ser Ala		
2565	2570	2575
Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val		
2580	2585	2590
Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala		
2595	2600	2605
Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn		
2610	2615	2620
Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser		
2625	2630	2635
Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp		
2645	2650	2655
Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly		
2660	2665	2670
Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu		
2675	2680	2685
Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln		
2690	2695	2700
Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn		
2705	2710	2715
Arg Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr		
2725	2730	2735
Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn		
2740	2745	2750
Glu Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser		
2755	2760	2765
Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe		
2770	2775	2780

<u>Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala</u>		
2785	2790	2795
<u>Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg</u>		
2805	2810	2815
<u>Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys</u>		
2820	2825	2830
<u>Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val</u>		
2835	2840	

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: ral2(yeast)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Gly Ala Lys Gly Leu Gln Leu Arg Ala Leu Arg Arg Ile Ala			
1	5	10	15

Arg Ile Glu Gln Gly Gly Thr Ala Ile Ser Pro Thr Ser Pro Leu			
20	25	30	

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: m3 (mAChR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys Arg Thr Lys Glu Leu  
1                   5                   10                   15

Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu Thr Glu  
20                   25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: MCC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu  
1                   5                   10                   15

Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu Thr Ala Met  
20                   25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATCAAGAC TGTGACTTTT AATTGTAGTT TATCCATT

40

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTAGAATT CATGTTAATA TATTGTGTT C TTTTAACAG

40

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTAGATTTA AAAAGGTGTT TTAAAATAAT TTTTAAGCT

40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCAATTGT TGTATAAAAA CTTGTTTCTA TTTTATTTAG

40

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTAACTTTTC TTCATATAGT AACATTGCC TTGTGTACTC

40

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

NNNNNNNNNN NNNNGTCCCTT TTTTTAAAAAA AAAAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAAGTAACT TGGCAGTACA ACTTATTGAACTTTAATA

40

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACAAGATA TTGATACTTT TTTATTATTT GTGGTTTTAG

40

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTTACT TGTTCTAAG TGATAAAACA GYGAAGAGCT

40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATAAAAACA TAACTAATTA GGTTTCTTGT TTTATTTTAG

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTAGTAAAT TSCCTTTTT GTTTGTGGGT ATAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCATTTTG CATGTACTGA TGTAACTCC ATCTAACAG

40

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTAAATAAAT TATTTTATCA TATTTTTAA AATTATTTAA

40

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATGATGTTA TCTGTATTTA CCTATAGTCT AAATTATAACC ATCTATAATG TGCTTAATTT

60

TTAG

64

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTAACAGAAG ATTACAAACC CTGGTCACTA ATGCCATGAC TACTTGCTA AG

52

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGATATTAAA GTCGTAATT TGTTTCTAAA CTCATTTGGC CCACAG

46

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTATGTTCTC TATAGTGTAC ATCGTAGTGC ATGTTCAAA

40

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCATTGCT CTTCAAATAA CAAAGCATTA TGGTTTATGT TGATTTTATT TTTCAG

56

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTAAGACAAA AATGTTTTT AATGACATAG ACAATTACTG GTG

43

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAGATGATT GTCTTTTCC TCTTGCCCTT TTTAAATTAG

40

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTT ATAACATGTA TTTCTTAAGA TAGCTCAGGT ATGA

44

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTGGCTTC AAGTTGNCTT TTTAATGATC CTCTATTCTG TATTTAATT ACAG

54

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACTATTAA GAATTCACC TGTTTTCTT TTTTCTCTTT TTCTTGAGG CAGGGTCTCA

60

CTCTG

65

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAACTAGTA TGATTTTATG TATAAATTAA TCTAAAATTG ATTAATTCC AG

52

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTACCTTGAA AACATTTAG TACTATAATA TGAATTTCAT GT

42

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCAACTCNAATTAGATGACC CATATTAGA AACTTACTAG

40

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATATAG AGTTTTATAT TACTTTAAA GTACAGAATT CATACTCTCA AAAA

54

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATTGTGACCT TAATTTGTG ATCTCTTGAT TTTTATTTC G

41

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCCCGCCTG CCGCTCTC

18

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAGCGGCCGG CTCCCGTG

18

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAACGGCT CTCATGCTGC

20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGTGCGGGG AGGAATGGA

19

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGATATCTT ACCAAATGAT ATAC

24

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATTCCTAC TTCTTCTATA CAG

23

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACCCATGCT GGCTTTTT C

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGGGCCATC TTGTTCCCTGA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTAGGCA CAAAGCTTGC AA

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCAAGCTCC AGTAAGAAGG TA

22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGCGGCTCCT GGGTTGTTG

19

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCCCCTTCCT TTCTGAGGAC

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTTCTCCTG CCTCTTACTG C

21

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGACACCCC CCATTCCCTC

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCACTTAAAG CACATATATT TAGT

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTATGGAAAA TAGTGAAGAA CC

22

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCTTAAGTC CTGTTTTCT TTTG

24

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTTAGAACCT TTTTTGTGTT GTG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCAGATTAT ACACTAAGCC TAAC

24

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CATGTCTCTT ACAGTAGTAC CA

22

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGGTCCAAGG GTAGCCAAGG

20

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAAAAATGGA TAAACTACAA TTAAAAG

27

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAATACAGAA TCATGTCTTG AAGT

24

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACACCTAAAG ATGACAATT GAG

23

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAACTTAGAT AGCAGTAATT TCCC

24

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACAATAAACT GGAGTACACA AGG

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATAGGTCATT GCTTCTTGCT GAT

23

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGAATTAA TGGATTACCT AGGT

24

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTTTTTTGCG TTTTACTGAT TAACG

25

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TGTAATTCA TTTATTCCTA ATA[G]CCTC

27

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTAGCCATA GTATGATTAT TTCT

24

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTACCTATT TTATACCCAC AAAC

24

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAAAGCCT ACACCATTTC TGC

23

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCATTCTT AGAACCATCT TGC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCTATAGTC TAAATTATAC CATC

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTCATGGCAT TAGTGACCAG

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

AGTCGTAATT TTGTTTCTAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGAAGGACTC GGATTCAC [G] C

21

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCATTCACTC ACAGCCTGAT GAC

23

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCTTGAAAC ATGCACTACG AT

22

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AAACATCATT GCTCTTCAAA TAAC

24

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TACCATGATT TAAAAATCCA CCAG

24

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATGATTGTC TTTTCCTCT TGC

23

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGAGCTATC TTAAGAAATA CATG

24

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTTTAAATGA TCCTCTATTG TGTAT

25

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACAGAGTCAG ACCCTGCCTC AAAG

24

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTCTATTCT TACTGCTAGC ATT

23

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 22 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATACACAGGT AAGAAATTAG GA

22

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 22 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TAGATGACCC ATATTCTGTT TC

22

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAATTAGGTC TTTTGAGAG TA

22

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTACTGCAT ACACATTGTG AC

22

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTTTTGTT TCCTAACATG AAG

23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCCACAG GTAATACTCC C

21

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCTAGAACTG AATGGGGTAC G

21

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAGGACAAAAA TAATCCTGTC CC

22

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTTTCTTAG TTTCATTCTT CCTC

24

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGAAGGATCCCTTGTGCAGTGTGGA

24

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

GACAGGATCCTGAAGCTGAGTTTG

24

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCAGAAAGTGCTGAAGAG

18

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGAATAATTAGGTCTCCAA

19

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAATCCTAACAGAGAGAACAA

21

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATGGCAAGCTTGAGCCAG

19

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTTCCAGCAGTGTACAG

18

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGAGATTCGCTCCTGA

102

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AGTACAAGGA TGCCAATATT ATG

23

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ACTTCTATCT TTTTCAGAAC GAG

23

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATTTGAATAAC TACAGTGTAA CCC

23

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CTTGTATTCT AATTGGCAT AAGG

24

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGCCCATAC ACATTCAAAC AC

22

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTTTGCGTC TTGCCATCT T

21

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AGTCTTAAAT ATTCAAGATGA GCAG

24

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTTCTCTTC ATTATATTCT ATGCTA

26

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AAGCCTACCA ATTATAGTGA ACG

23

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AGCTGATGAC AAAGATGATA ATC

23

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAGAAACAAT ACAGACTTAT TGTG

24

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATGAGTGGGG TCTCCTGAAC

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATCTCCCTCC AAAAGTGGTG C

21

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TCCATCTGGA GTACTTTCTG TG

22

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGTAAATGCT GCAGTCAGA GG

22

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCGTGGCATA TCATCCCC

19

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCCAGACTGC TTCAAAATTA CC

22

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAGCCTCATC TGTACTTCTG C

21

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CCCTCCAAT GAGTAGCTG C

21

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TTGTGGTATA GGTTTACTG GTG

23

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ACCCAACAAA AATCAGTTAG ATG

23

(2) INFORMATION FOR SEO ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GTGGCTGGTA ACTTTAGCCT C

21

(2) INFORMATION FOR SEO ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATGATGTTGA CCTTTCCAGG G

21

(2) INFORMATION FOR SEO ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATTGTGTAAC TTTTCATCAG TTGC

24

(2) INFORMATION FOR SEO ID NO:127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AAAGACATAC CAGACAGAGG G

21

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTTTTTTGGC ATTGCGGAGC T

21

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

AAGATGACCT GTTGCAGGAA TG

22

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATCAGACC AAGCTTGTCT AGAT

24

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CAATAGTAAG TAGTTACAT CAAG

24

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

AAACAGGACT TGTACTGTAG GA

22

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CAGCCCCCTTC AAGCAACAT C

21

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAGGACTTAT TCCATTCTA CC

22

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CAGTCTCCTG GCCGAAACTC

20

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTTGACTGGC GTACTAATAC AG

22

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TGGTAATGGA GCCAATAAAA AGG

23

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

TGGGACTTTT CGCCATCCAC

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TGTCTCTATC CACACATTG TC

22

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ATGTTTTCA TCCTCACTTT TTGC

24

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGAGAAGAAC TGGAAGTTCA TC

22

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(vi) ORIGINAL SOURCE:  
(A) Homo sapiens  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGAATCTTT AATGTTGGGA TTTGC

25

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(vi) ORIGINAL SOURCE:  
(A) Homo sapiens  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCTCCCACAG GTAATACTCC C

21

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(vi) ORIGINAL SOURCE:  
(A) Homo sapiens  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GCTACAACTG AATGGGGTAC G

21

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CAGGACAAAA TAATCCTGTC CC

22

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ATTTTCTTAC TTTCATTCTT CCTC

24

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Artificial sequence (consensus)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Phe Xaa Val Glu Xaa Thr Pro Xaa Cys Phe Ser Arg Xaa Ser Ser Leu Ser Ser Leu  
1 5 10 15

Ser

20

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Tyr	Cys	Val	Glu	Asp	Thr	Pro	Ile	Cys	Phe	Ser	Arg	Cys	Ser	Ser	Leu
1															15
Ser	Ser	Leu	Ser												
															20

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

His	Thr	Val	Gln	Glu	Thr	Pro	Leu	Met	Phe	Ser	Arg	Cys	Thr	Ser	Val
1															15
Ser	Ser	Leu	Asp												
															20

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Phe	Ala	Thr	Glu	Ser	Thr	Pro	Asp	Gly	Phe	Ser	Cys	Ser	Ser	Ser	Leu
1															15
Ser	Ala	Leu	Ser												
															20

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Tyr	Cys	Val	Glu	Gly	Thr	Pro	Ile	Asn	Phe	Ser	Thr	Ala	Thr	Ser	Leu
1					5								10		15
Ser	Asp	Leu	Thr												
				20											

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Thr	Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe	Ser	Arg	Asn	Asp	Ser	Leu
1					5								10		15
Ser	Ser	Leu	Asp												
				20											

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Phe	Ala	Ile	Glu	Asn	Thr	Pro	Val	Cys	Pro	Ser	His	Asn	Ser	Ser	Leu
1					5								10		15
Ser	Ser	Leu	Ser												
				20											

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Arg	His	Val	Glu	Asp	Thr	Pro	Val	Cys	Phe	Ser	Arg	Asn	Ser	Ser	Leu
1					5					10					15
Ser	Ser	Leu	Ser												
					20										